# Bioinformational diplomacy: global health emergencies, data sharing and sequential life

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# Bioinformational diplomacy: Global health emergencies, data sharing and sequential life

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## Abstract

Global health emergencies – like COVID-19 – pose major and recurring threats in the 21st century. Now societies can be better protected against such harrowing outbreaks by analysing the detailed genetic sequence data of new pathogens. Why, then, is this valuable epistemic resource frequently withheld by stakeholders – hamstringing the international response and potentially putting lives at risk? This article initiates the social scientific study of bioinformational diplomacy, that is, the emerging field of tensions, sensitivities, practices and enabling instruments surrounding the timely international exchange of bioinformation about global health emergencies. The article genealogically locates this nascent field at the intersection of molecularised life, informationalised biology and securitised health. It investigates the deeper political, economic and scientific problematisations that are engendering this burgeoning field. It finally analyses the emergent international instruments developed by governments, scientists and industry to facilitate more rapid global sharing of bioinformation through novel practices of data passporting. Overall, the in-depth study of bioinformational diplomacy reveals just how deeply, and even constitutively, international relations are entangled with the life sciences – by carefully tracing how laboratory practices of sequencing life at molecular scale also end up recontouring the play of sovereignty, power and security in international relations.

## Keywords

health security, diplomacy, science, biopolitics, global health, data sharing

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## Introduction

New infectious disease outbreaks continue to pose a major and recurring global challenge in the 21st century (Davies and Wenham, 2020; Harman, 2012; Lakoff, 2017; Youde, 2020).[1] An initially localised outbreak – like COVID-19 – can quickly spread across the entire world, killing millions in the process and infecting tens of millions more. As with many other recent outbreaks – like pandemic flu, Middle East respiratory syndrome (MERS), Ebola and Zika – such global health emergencies bring harrowing devastation to lives, livelihoods and economies all around the planet (WHO, 2019). Yet advances in science and technology are also creating powerful new ways to better protect populations against this harmful epidemic of epidemics. Specifically, the ability to scientifically analyse the detailed genetic sequence information of new pathogens can today significantly accelerate risk assessments, help formulate evidence-based responses and stimulate the rapid development of life-saving medical interventions. These vital benefits can all accrue provided that key stakeholders located around the world – especially scientists, governments and the pharmaceutical industry – rapidly exchange this valuable pathogen genetic sequence data as it becomes newly generated during outbreaks. Yet despite a powerful global health rationale, as well as repeated calls by influential bodies like the World Health Organisation (WHO), the rapid international sharing of pathogen sequence data has proved difficult to achieve during recent outbreaks – repeatedly hampering the global response and potentially putting lives at risk (Littler et al., 2017; WHO, 2015). That data-sharing conundrum sits at the heart of an emerging field of practice that is captured, explored and analysed in greater detail below.

This nascent field of practice is forming because of a critical change in the way that global health emergencies are managed now. In the past, scientists investigating outbreaks were still overwhelmingly reliant upon physically examining biological specimens of a novel pathogen. This usually meant that scientists would have to wait for quite some time before such dangerous samples were first shipped safely from outbreak countries (frequently located in the Global South), to leading scientific laboratories (often situated in high-income countries). Today, by contrast, scientists are far less dependent upon receiving those biological materials. Transformative advances in sequencing technology, molecular biology and bioinformatics mean that scientists can increasingly use information technology to perform much of this time-sensitive work virtually and computationally – just by rapidly analysing a pathogen's digital sequence data, which contains the order of the four chemical building blocks (or bases) making up DNA/RNA molecules (García-Sancho, 2012). As sequencing technology becomes ever more powerful, affordable and portable, such pathogen sequence data can be generated in near 'real-time' during global health emergencies, and some epidemiologists are already taking mobile sequencing equipment directly to the source of new outbreaks (Gardy et al., 2015; Shaw and Sugden, 2018).

Despite the growing centrality of pathogen genetic sequence data for managing global health emergencies, however, social scientists outside of the community of sequencing professionals know surprisingly little about the social processes through which such pathogen sequence data are acquired, exchanged and circulated (or not) internationally (Wellcome Trust, 2018: 2). There has been no systematic social scientific exploration of this emerging field of international sequence data sharing to date – only a patchwork of

anecdotal accounts, editorials, blogs, case studies, ad-hoc initiatives, think-tank reports and newspaper articles clustered around particular outbreaks. What obstacles are hindering the timely international sharing of bioinformation about global health emergencies? How do the requirements of such *informational* exchanges differ in comparison to older forms of sharing biological specimens? What, moreover, are the new infrastructures emerging to make this bioinformation flow more quickly between stakeholders located all around the world?

This article develops a new analytical framework to initiate the in-depth investigation of that emergent field of practice: bioinformational diplomacy. Bioinformational diplomacy can be defined as the emerging field of tensions, sensitivities, practices and enabling instruments surrounding the timely international exchange of bioinformation about global health emergencies. The core problematisation residing at the centre of this emerging field is how critical bioinformation can be quickly shared internationally for the purposes of better managing lethal infectious disease outbreaks. Bioinformational diplomacy thus comporises three constituent elements. First, it encompasses the broad array of actors and technologies variously involved in generating, exchanging, utilising or otherwise bearing upon the international flow of such bioinformation – especially (but by no means restricted to) governments, scientists and industry. Second, it is constituted by a multifaceted set of political, security, commercial and professional sensitivities surrounding such bioinformation – leading to protracted data-sharing barriers and frequently culminating in a potentially dangerous form of global epistemic friction. Finally, this emergent field also comprises the novel practices and instruments (both formal and informal) being designed now by those stakeholders to facilitate more rapid international sharing of bioinformation for future global health emergencies.

Overall, the in-depth study of bioinformational diplomacy reveals how bioinformation is becoming increasingly critical to the international play of power, commerce and security in contemporary world politics – requiring us to broadly re-think international relations also as informational relations. It further reveals that beneath the purview of formal intergovernmental diplomacy widely studied in International Relations, there also lurks another thick layer of informal epistemic diplomacy routinely undertaken by scientists in the course of their professional work. Scientists, too, are informal diplomatic actors continuously engaging in infra-diplomatic practices to globally source valuable knowledge resources across potentially sensitive international and geopolitical divides. Finally, the study of bioinformational diplomacy also fundamentally challenges the notion that international relations and the life sciences can be thought of as largely distinct fields. It reveals, rather, how the laboratory practices of sequencing life at tiny molecular scale also cascade upwards into the macro-play of sovereignty, power and security in international relations. The relationship between the life sciences and international relations must, therefore, be considered one of deep constitutive entanglement.

## *Bioinformational diplomacy: the new management of global health emergencies*

The management of global health emergencies is changing in the 21st century (WHO, 2021: 2). Whereas historically scientists investigating any new outbreak needed

to examine biological samples of a new pathogen, such scientific investigation can increasingly be performed computationally just by analysing a pathogen's genetic sequence data. As Bronwyn Parry argues more generally, 'the molecularisation of biological research has transformed approaches to the study of diseases and pharmaceutical development. While researchers are still interested in examining specimens morphologically, these examinations are now, almost without exception, undertaken in concert with analyses of the genetic or biochemical composition' (Parry, 2004: 5). Since that observation was penned, technological advances have continued apace, meaning that in some cases genetic sequence data is already interchangeable with physical specimens. The genetic sequence data of lethal pathogens are therefore also becoming far more central to the international management of new outbreaks.

Already scientific analysis of such sequence data can improve the international response to global health emergencies in three key ways. First, sequence data can accelerate the completion of risk assessments by helping scientists to quickly characterise a new pathogen, understand its virulence, identify its likely natural reservoir, and evaluate the overall threat it poses (Wellcome Trust, 2017: 4; WHO, 2018). During the Ebola outbreak in West Africa, for example, pathogen sequence data 'revealed critical insights into the origins of infection and the evolution and transmission of the disease' (Wellcome Trust, 2017: 4). During the COVID-19 outbreak, moreover, genetic sequencing practices quickly allowed Chinese scientists to determine that the outbreak was caused by a new coronavirus (SARS-CoV-2), and to map the complete genetic sequence of this new virus in a matter of just days.

Second, sequence data enables scientists to virtually perform molecular epidemiology by comparing the detailed sequences of many different viruses, thereby tracing where, how and how quickly a new virus is spreading geographically. During the recent outbreaks of Ebola and SARS-CoV-2, for instance, analysis of sequence data allowed tracking of their spatio-temporal spread and it showed 'how different strains crossed borders and spread within countries', allowing for evidence-based 'border closures to limit its spread (Gardy et al., 2015; Marston et al., 2017; Wellcome Trust, 2017: 4; WHO, 2017: 2). Increasingly, analysis of such sequence data can also assist with inferring a pathogen's basic reproductive number, as well as identifying more dangerous new strains that emerge over the course of a pandemic (WHO, 2021: 3). This aids governments in better calibrating their responses, and in formulating evidence-based decisions about how to allocate limited public health resources.

Finally, sequence data can be harnessed for the development of new medicines, vaccines, and diagnostics (Yozwiak et al., 2015). During a 2013 outbreak of deadly human infections with H7N9 influenza in China, for example, scientists in the United States used genetic sequence data to artificially synthesise new virus genes in a matter of days, and then worked with vaccine manufacturers to rapidly develop a new H7N9 vaccine without needing recourse to a biological sample (Dormitzer et al., 2013; Shu and McCauley, 2017). This dynamic has continued apace through to COVID-19, where the use of sequence data is now leading to the rapid development of new genetic diagnostics as well as the identification of molecular targets for new vaccines and antiviral medications (WHO, 2021: x.). Already the scientific analysis of pathogen genetic sequence data therefore harbours immense potential for better protecting populations against the harmful effects of global health emergencies.

Yet all those attempts to harness the nascent scientific power of pathogen sequence data also confront one major obstacle. These vital benefits can only accrue if key stakeholders located around the world – especially scientists, governments and the pharmaceutical industry – readily exchange all of this pathogen sequence data as it becomes newly generated in many different countries. The scientific value of pathogen sequence data is mostly realised at the point that those data are collectively pooled and compared in a large bioinformational database, making the widespread international sharing of such data critical (Gardy et al., 2015; Johnson and Parker, 2019). It is imperative, moreover, that stakeholders also share these data very *rapidly* because '[s]peed is everything' during an outbreak (Schatz and Phillippy, 2012; Yozwiak et al., 2015).

Yet this powerful global health rationale notwithstanding, recent outbreaks have repeatedly struggled to achieve such rapid international sharing of pathogen sequence data (WHO, 2016a). During the first SARS outbreak in 2002–3, for example, only three virus genomes were publicly shared in the first month following identification of the causative agent, and only 31 had become available within the first three months (WHO, 2021: 2). A decade later, during the 2012 outbreak of Middle East respiratory syndrome (MERS), efforts to understand its origins and source were still hampered for several years because of inadequate data sharing (McNabb et al., 2014). The Ebola outbreak in West Africa (2013–16) again highlighted 'the deficiencies with existing data-sharing mechanisms' (Dye et al., 2016); and there even 'was three months of stasis, during which no new virus sequence information was made public' (Yozwiak et al., 2015). This situation had not improved much by the time of the Zika outbreak of 2015, during which data-sharing issues again 'highlighted major deficiencies in knowledge of the virus and disease' (Chretien et al., 2016; Saez, 2016). Despite some notable successes, these outbreaks have all been marked by significant withholding of data. That has 'been bad for science and almost certainly bad for health' (Pisani et al., 2016) – with potentially 'disastrous public health consequences, leading to unnecessary suffering and death' (Modjarrad et al., 2016). There is thus an urgent need to better understand the tensions and practices surrounding the global exchange of this vital epistemic resource.

The analytical framework of bioinformational diplomacy developed here can help to initiate the social scientific exploration of that crucial field of practice. This approach differs from discussions about data-sharing taking place in the fields of the life sciences and global health, where data-sharing tends to be construed largely as a technical and/or functional challenge. The novel framework of bioinformational diplomacy proposed here, by contrast, seeks to understand the global sharing of pathogen sequence data as an international political challenge, and even as an inherently *diplomatic* one. At least three aspects endow this burgeoning field with such a decidedly diplomatic inflection. First, the field involves the urgent, international and cross-border exchange of information between actors who are geographically located in different states, thus cutting across multiple sovereign jurisdictions. Second, and as we will see in more detail below, those sequence data also become politically and commercially very sensitive amidst all the heightened international political pressures of an acute outbreak – precisely because of the critical role they now play in risk assessment, outbreak response and the development of life-saving medical interventions. Third, effecting the timely international exchange of bioinformation amidst all those acute international political pressures of an unfolding

global health emergency therefore requires quite careful and tactful negotiation between powerful stakeholders. This trilogy – of international movement, highly sensitive information and skilful negotiation – ultimately render the international sharing of pathogen sequence data about global health emergencies more than just a technical, or even a political, challenge; it also becomes a fundamentally *diplomatic* one. Overall, this novel approach thus aims to bring deeper social scientific inflection to the analysis of data-sharing by explicitly teasing out some of the subtler political, economic and security dynamics involved in passaging digital sequence data across diverse sovereign, geopolitical and North–South divides.

Conceptually, this new framework of bioinformational diplomacy builds upon two concurrent fields of study. On the one hand, the notion is informed by recent scholarship on diplomacy. Much of this diplomacy scholarship already goes well beyond the traditional imaginaries of high-level intergovernmental negotiations and grand diplomatic dramas of war and peace that long defined the field (Constantinou and Derian, 2010; Sending et al., 2011). Multiple studies now point to the growing diplomatic significance of non-state actors, as well as their informal diplomatic practices that increasingly characterise the more open, networked and less state-centric multilateralism of the 21st century (Heine, 2008; Langenhove, 2016a; Slaughter, 2019). These include studies of para-diplomacy (Aldecoa and Keating, 2013; Kuznetsov, 2015), transprofessional diplomacy (Constantinou et al., 2016), everyday diplomacy (Dittmer, 2015; Marsden et al., 2016), science diplomacy (Kaltofen and Acuto, 2018; Langenhove, 2016b), global health diplomacy (Davies et al., 2015; Katz, 2009), private diplomacy (Scott-Smith, 2014), grassroots diplomacy (Hinton et al., 2014; Payne, 2009) and data diplomacy (Jacobson et al., 2018). Building upon this body of scholarship, the notion of bioinformational diplomacy similarly operates with such a broader understanding of diplomacy that encompasses both *formal* inter-governmental negotiations occurring in diplomatic fora (such as the World Health Organization or the Convention on Biodiversity), as well as many *informal* practices also widely utilised by non-state actors (like scientists and industry) to internationally exchange such data.

At the same time, this framework of bioinformational diplomacy builds upon recent social studies of science and technology, especially the rise of molecular biology as a powerful force within society, global health and international relations (Cooper, 2008; Dillon, 2015; Dillon and Reid, 2009; Elbe, 2014; Howell, 2014; Long, 2019). Particularly salient here is the concept of *bioinformation* recently defined by Bronwyn Parry and Beth Greenhough as ‘all information, no matter how constituted, arising from analyses of biological organisms and their behaviour, that can be used to elucidate their structure or function, identify individuals, or differentiate them from each other’ (Parry and Greenhough, 2017: 8). Bringing together the broadening study of diplomacy and the social scientific study of molecular biology, the framework of bioinformational diplomacy proposed here thus begins to analytically capture how the international passaging of bioinformation about global health emergencies is rapidly emerging as a distinct field of formal and informal diplomatic practice in the international system. This nascent domain of bioinformational diplomacy can be summarily defined as the emerging field of tensions, sensitivities, practices and enabling instruments surrounding the timely international exchange of bioinformation about global

health emergencies. It conceptually delineates that crucial space in contemporary world politics where the molecular biopolitics of genetic sequencing begin to directly intersect with the geopolitical dynamics of sovereignty, power and security.

## *Making the cut molecularly: the onto-epistemology of sequential life*

The international rise of bioinformational diplomacy is part of a broader biopolitical reconfiguration – one in which 'life' itself is coming to be understood more *sequentially* in the 21st century. Three intersecting developments drive the genealogical emergence of this field: the molecularisation of life, the informationalisation of biology, and the securitisation of health. First and foremost, bioinformation (like genetic sequence data) is premised upon the idea that life is fundamentally driven by biochemical processes unfolding at *molecular* scale. The granularity at which we can understand and imagine biological life has shrunk considerably over the course of the 20th century – moving first from the corporal body to the inner workings of the cell, and eventually advancing all the way to the scale of individual atoms embedded in their respective molecular groupings. Scientific techniques like x-ray crystallography have since allowed the precise molecular structure of DNA to be revealed. As double Nobel Prize winner Frederick Sanger once put it, DNA 'contains the whole information for the development of an organism, coded in the form of sequences of the four nucleotide residues' (cited in García-Sancho, 2012: 60). The French biochemist and Nobel prize winner Jacques Monod expressed this biochemical understanding of life particularly succinctly when he later proclaimed that all 'living beings are chemical machines' (Monod, 1997: 51). That moves biopolitics considerably beyond Foucault's original conception of biopower operating at the level of the body and the population, and pushes the management of 'life' towards a deeper form of molecular biopower (Elbe, 2014, 2018; Long, 2019).

Yet this molecular vision of life is merely a necessary, and not a sufficient, condition for the rise of bioinformational diplomacy. Equally critical is a second process through which these chemical building blocks then also come to be seen as forming a complex system of information – a kind of metaphorical code. DNA could thus be rendered into a fairly simple, if also very long, text made up of only four characters (Gs, Cs, As, and Ts), with the resulting string of letters appearing 'as a kind of language or expressed information' (Parry and Greenhough, 2017: 3–4). This 'informationalisation' of molecular biology also entails a crucial process of de-corporalisation in which information effectively 'loses its body' (Hayles, 1999). Once generated, genetic sequence data retain virtually no degree of corporality at all: 'all the body of the thing has been divested in the interest of rendering it in a more purely informational form – as data or image' (Parry, 2004: 65). That also makes DNA sequences much more 'lightweight and transmissible', as well as 'easier to convey from one location to another' (Parry, 2004: 60). With the aid of computers and related information technologies (see García-Sancho, 2012; Stevens, 2011, 2013), this informational turn in biology enables scientists to study new pathogens virtually now, without having to first wait for tedious and bureaucratic shipments of biological materials. The informationalisation of biology is therefore a second key development driving the genealogical rise of bioinformational diplomacy.

This confluence of the 'molecular' and the 'informational' has been sufficiently powerful to trigger a wider biopolitical reconfiguration – effectively engendering a new understanding of life as an elaborate biochemical information system (Kay, 2000: 1). 'Life' itself is becoming increasingly understood as a complex flow of molecular *information* (see also Braun, 2007; Galloway and Thacker, 2007; Hester, 2016; Rose, 2006). The feminist philosopher of science Karen Barad advances the notion of an onto-epistemology to signal the inherent inseparability of ontology and epistemology when it comes to knowing and understanding the world (Barad, 2007: 409). Such a novel onto-epistemological entanglement is arguably also at play in the rise of genetic sequence data. Understanding life as sequence entails profound ontological commitments – viewing life as being fundamentally bio-chemical in nature. Yet it is simultaneously an *epistemology*, because it further asserts that life can now be 'read' and 'known' through detailed analysis of genetic sequences. Ultimately, the rise of genetic sequence data is thus part of a whole new way of understanding and knowing – or 'cutting' into – life sequentially: *sequential life.*

Yet there is also a third dynamic critical for understanding the rise of bioinformational diplomacy. In the absence of an acute sense of danger, urgency and existential threat, it would not be such a pressing matter whether all this new bioinformation is exchanged globally, how widely it circulates or indeed how quickly it is exchanged. During normal times, those questions could largely remain a more routine matter of technical or functional cooperation between stakeholders. All of this changes very quickly, however, amidst the securitised political context of a new lethal outbreak. During those exceptional periods, it does suddenly become a potential matter of life and death whether this data flow widely and rapidly – especially now that a number of vaccine manufacturers are already using genetic sequence data as an alternative way to develop new medical interventions (Roemer-Mahler and Elbe, 2016; WHO, 2014: 4; Yozwiak et al., 2015). Global health emergencies thus generate particularly intense stressors around the international circulation of bioinformation – elevating the question of its global exchange beyond the technical or even political spheres and transforming it into an inherently diplomatic issue as well. Ultimately, then, the nascent field of bioinformational diplomacy is forming at the genealogical conjuncture of three distinct developments – molecularised life, informationalised biology *and* securitised health. To study such bioinformational diplomacy, moreover, is to essentially investigate the emergent *global politics of sequential life* – that is, to trace how the molecular biopolitics of sequential life are beginning to rub up against the geo-political dynamics of sovereignty, power and security in international relations (see also Constantinou and Opondo, 2019).

## *Epistemic friction: Barriers to data sharing during global health emergencies*

What wider sensitivities traverse the emergent field of bioinformational diplomacy? Many leading scientists involved in early sequencing efforts hoped that all such newly-generated data would be made freely, publicly and quickly available to everyone around the world. A new repository to openly share such new genetic sequence data – called GenBank – was even established for this very purpose as early as 1982

(Choudhuri, 2014: 80). Historically, GenBank is therefore closely associated with the open science movement and the 'Bermuda Principles'. The latter were proposed by the scientist John Sulston during the Human Genome Project (HGP), which culminated in the first successful sequencing of the entire human genome (Hilgartner, 2017; Stevens, 2015). Under those Bermuda Principles the leading genome-sequencing centres involved in the international effort committed themselves to depositing gene sequences – every 1,000 base pairs – into GenBank within 24 hours of completing their work (So, 2012). Doing so would allow rapid and open international access to the data; but it would equally ensure that such sequence data remained a public good by preventing others from trying to exert intellectual property rights over such data. 'The best way to prevent the sequence being carved up by private interests', Sulston argued, 'was to put it into the public domain so that, in patent office jargon, as much as possible became "prior art" and therefore unpatentable by others' (Ferry and Sulston, 2002: 300). That is also why GenBank does not place any further restrictions upon the use of the genetic sequence data deposited in its database and anyone with access to the internet can freely and anonymously download the sequence data contained within it (GenBank, 2019).

Those initial scientific aspirations for timely, open and unrestricted sharing of genetic sequence data soon came under considerable international political pressure however, especially amidst new infectious disease outbreaks. In 2003, for example, models of open data sharing quickly ran into difficulties when new human infections with a lethal H5N1 ('bird' flu) virus were detected in Asia, triggering international concern that the world was on the cusp of a devastating new 'bird' flu pandemic. The rapid transition towards this more securitised international political context intensified numerous underlying tensions surrounding pathogen sequence data and impeded much of its open sharing. It quickly became apparent that some governments experiencing H5N1 outbreaks were unwilling for this sensitive sequence data to be made publicly available; and they also voiced concerns about losing intellectual property potentially attached to such sequences. WHO engaged in diplomatic efforts to address those concerns by creating a separate password-protected database at the Los Alamos National Laboratory in the United States, which could only be accessed by a select number of scientists from approximately fifteen of the world's leading laboratories. This move was quickly met with resistance from other scientists, however, who argued that without access to those data they could no longer carry out their work properly and contribute to pandemic preparedness efforts. Thus, the imminent threat of an H5N1 pandemic threat quickly put immense strain upon the whole system of open sequence data sharing and it revealed that during such outbreaks all three of the key stakeholders – scientists, government and industry – also harbour deeper sensitivities about the international sharing of such pathogen sequence data.

Pathogen sequence data are sensitive because they sit at the heart of multiple global chains of value production. Scientists generating new pathogen sequence data during a major international outbreak, for example, may not wish to share them rapidly because their career standing and progression have long been measured by publications and citations. Scientists working on a new pathogen can thus become concerned that rapidly sharing their data would allow a competing scientist to easily 'scoop' them by using that same data to publish more quickly (Chretien et al., 2016; Pearson, 2003). Scientists at the

forefront of new outbreaks suddenly also become extremely busy, as their laboratories go into overdrive and they often do not have enough resources to meet this surge in demand. Historically, some scientists have therefore decided to share virus sequence information in public databases only *after* their scientific articles had been accepted for publication – leading to delays of several months to the potential detriment of global health (Edelstein, 2015: 12; Noor et al., 2006). There is also a critical North–South dimension involved here. Scientists from low- and middle-income countries, where many outbreaks have historically occurred, frequently lament that analyses from samples they shared in the past have subsequently been presented at international meetings and scientific conferences without proper advance notification, or without including those who had shared the samples in the authorship arrangements (Bockarie, 2019; Sedyaningsih et al., 2008). One set of tensions surrounding pathogen sequence data thus pertain to how, and how equitably, the career/research benefits generated from those data are subsequently distributed among different scientists.

During acute international outbreaks, these longstanding problem of global scientific rivalry and disparity also begin to intersect with wider international political and economic sensitivities. Governments too may have reasons for restricting the international sharing of sequence data, even when scientists would otherwise be prepared to share it. The wider circulation of the data could have negative economic ramifications that governments are sensitive about – especially if travel to such countries is curtailed and trade is interrupted as a result (Aarestrup and Koopmans, 2016: 243; Centre for Evidence Based Medicine, 2015). Conversely, such sequence data could also lead to the development of life-saving (and commercially highly lucrative) new medical countermeasures – like diagnostics, vaccines or antiviral medications (Hester and Williams, 2020). Intellectual property can thus become another significant barrier here, as governments may feel that by sharing such data they are placing something with potentially considerable commercial value into the public domain (Hilberg, 2015; Pottage, 2006: 150). Governments must, furthermore, consider the national security implications of handling such dangerous sequences, especially in light of their potential role in the development of novel bioweapons (Gostin et al., 2014). Because of those heightened political sensitivities around the commercial and security ramifications of pathogen sequence data, some governments now require their scientists to first seek formal permission before sharing such data on viruses with pandemic potential, creating another potential barrier (WHO, 2016b: 16).

This entire field of pathogen sequence data sharing is, moreover, interspersed with longer standing tensions caused by the stark global health inequalities between high- and low-income countries (Robinson et al., 2013). Governments from low- and middle-income countries will be concerned to ensure that their populations too can secure access to any new medicines and vaccines produced with the help of such sequence data – as newly developed medical countermeasures may later turn out to be very costly, or only available in insufficient quantities (Centre for Evidence Based Medicine, 2015; Pearson, 2003), and also because of their formative historical experiences of extractive 'biopiracy' (Quaglia, 2016). This can lead to charges of 'biocolonialism' whereby 'valuable samples and data were expropriated to the metropolitan centres of the West for use in pharmaceutical development without any reciprocal benefits being returned to the source

communities . . ..' (Parry and Greenhough, 2017: 22), and some data-sharing practices can also be seen as extending historical practices of extraction into the present (see also Tilley, 2017). These longer-standing concerns about global equity and justice provoke further political tensions still around the international exchange of pathogen sequence data, ultimately generating a multifaceted vortex of professional, economic, security and equity sensitivities surrounding that data.

All of these diverse sensitivities help to explain why, a strong global health rationale notwithstanding, most major outbreaks over the past two decades have encountered entrenched barriers to the rapid international sharing of pathogen genetic sequence data. Scholars of 'big data' invoke the notion of 'data friction' to capture the wide array of socio-material factors that can restrict the movement of data including 'the relative power and influence of different actors who desire to shape the movement of data' (Bates et al., 2016: 8–9). The notion of data 'friction' thus acknowledges how, contrary to widespread perception, information does not always flow easily or naturally. Often a multiplicity of practical and political tensions have to first be overcome via concerted efforts (see also Jacobson et al., 2018); and data have to actively be made to move through a delicate patchwork of mechanisms, processes, incentives and infrastructures. Considering the experience with recent outbreaks, it is becoming evident that there are many such barriers also operating at international level, producing global epistemic friction that can hamstring the international response.

## *Data passporting: the Global Initiative for Sharing All Influenza Data (GISAID)*

What new instruments are being designed to improve the international sharing of pathogen sequence data for future global health emergencies? Over the past decade, several key stakeholders in the influenza field have begun experimenting with an alternative model of bioinformational diplomacy. Officially launched at the World Health Assembly (WHA) in 2008, the Global Initiative for Sharing All Influenza Data (GISAID) utilises a different model of data *licensing* to address the deeper sensitivities surrounding pathogen sequence data and as a way of providing data contributors with greater levels of protection about how others subsequently use that data.

This licensing model means that, in contrast to GenBank, users accessing pathogen sequence data through GISAID must first consent to a unique database access agreement (DAA) governing the data contained in its EpiFlu database. This unique data access agreement contains multiple binding stipulations, including that users will share their data with others in the GISAID network, but will *not* distribute such data to other non-GISAID users. Users must further agree to credit the use of others' data in their publications, to make best efforts to collaborate with the scientific laboratory from which the sequence data originated, and to involve them in research using the data. The agreement also commits users to maintain common access to any technology subsequently derived from such sequence data, so that it can be used for research and the development of diagnostics, medicines and vaccines. This last stipulation is aimed at preventing intellectual property assertions by industry (or others) that might subsequently make it more difficult for low-income countries to access new medical interventions (GISAID, 2011).

Use of this data access agreement does not mean that GISAID is abandoning the principle of a publicly accessible sequence database, because any person can still obtain credentials for accessing data through GISAID. It does mean, however, that GISAID prohibits anonymous access to the data in the way that GenBank does. GISAID instead requires all new users to initially undertake a one-time process of positive identification (GISAID, 2011). This identification mechanism makes it easier for scientists to discover, and properly acknowledge, those who originally contributed the data – improving 'sequence etiquette' and building greater trust in data sharing (Fearnley, 2020). That process of positively identifying the contributors and users of data also gives GISAID the basis to enforce the rules set forth in the database access agreement. In extreme cases, GISAID can even bar a user's access to the database, if they are seen to violate the terms of the database access agreement. Crucially, this licensing mechanism means that data deposited through GISAID also does *not* fall under the legal definition of 'public domain'. GISAID does not remove or waive any potential pre-existing 'rights' that might apply to such data; any ownership rights potentially surrounding the sequence data are therefore unaffected by virtue of being submitted to GISAID. Overall, GISAID's use of this alternative data licensing mechanism, in conjunction with its process of positive identification, thus provides an additional level of assurance to governments concerned about intellectual property, as well as to scientists worried about being 'scooped'.

In recent years, GISAID's alternative sequence data sharing model has become widely embraced by the global influenza research community. That includes the Global Influenza Surveillance and Response Systems (GISRS), which spans more than one hundred countries, monitors the global spread of influenza, and makes recommendations for the composition of the annual flu vaccines. GISAID has thus managed to attract a large volume of genetic sequence data on influenza viruses over the past decade, and now reportedly contains the most comprehensive collection of such high-quality influenza data in the world (Saez, 2016). Beyond *seasonal* influenza, moreover, GISAID has also begun to develop a track record in facilitating the sharing of sequence data about influenza viruses with human *pandemic* potential such as H5N1, H1N1 and H7N9 (ECDC, 2014; WHO, 2009). In the influenza field GISAID has therefore rapidly established itself as an alternative mechanism of bioinformational diplomacy and as a new international information infrastructure for (influenza) sequence data (see Bowker et al., 2019).

GISAID's ability to facilitate such increased international sharing of influenza genetic sequence data is largely due to how its licensing model places additional conditions and obligations around the handling of such data – a practice that might be called 'data passporting'. Data passporting can be understood here as the international counterpart to the notion of data structuring developed recently by scholars in the field of big data. Data structuring captures the 'configurations of digital traces that are organised and ordered in ways that allow for analysis, value extraction and connection to different forms of social activity such as commercial production or political advocacy' (Flyverbom and Murray, 2018: 2). The concept of data structures was thus developed to 'highlight how design choices, ways of sorting data and other dimensions of digital spaces create novel conditions for knowledge production and communication in general' (Flyverbom and Murray, 2018: 10). This notion of data structuring is particularly useful for capturing the significance of the *internal* conditioning of data within different information systems.

The comparative success of GISAID in the influenza field suggests, however, that the *external* conditioning of data can be just as significant, especially when it comes to facilitating its rapid international transmission. Much like passports have historically set out the conditions/obligations under which people can/cannot move across different countries and sovereign jurisdictions (see Salter, 2003), so too the key to GISAID's success in encouraging the greater international sharing of sequence data is closely tied to the wider envelope of legal and ethical obligations placed upon users in terms of how they access and subsequently use the data. The notion of data passporting proposed here captures this key difference between the *internal* and *external* configuration of data and it further highlights the growing significance becoming attached now to the external conditions placed upon bioinformation in order to facilitate its greater international dissemination and rapid cross-border passaging, particularly during acute outbreaks.

Yet this significant headway made by GISAID in the influenza field notwithstanding, many questions about international pathogen sequence data sharing still remain unresolved (Reardon et al., 2016). Although it is impossible to know for certain, it seems likely that even today a considerable amount of newly generated sequence data is still not being shared; and some countries also continue to share much more data than others. There is, moreover, a major gap that remains because many outbreaks – like MERS, Zika and Ebola – are not caused by influenza viruses. Here the outbreak of COVID-19 marked another critical test for the rapidly evolving field of bioinformational diplomacy. Chinese scientists were able to sequence the new virus within 72 hours, and notified WHO of a new outbreak on the last day of December 2019 (Xiaoyu, 2020). In early January, Chinese scientists then shared the first complete sequence of the new coronavirus on a new open access website called virological.org. They also deposited sequence data in GenBank and approached GISAID to see whether the platform would be willing to host sequence data about new coronavirus (Pandey, 2020). At that point GISAID decided, for the first time, to open up its sharing platform beyond influenza data and to include genetic sequence data about SARS-CoV-2 as well. This enabled scientists in other countries to quickly use such shared sequence data to begin the process of developing new diagnostics and vaccines for the virus (Fearnley, 2020). Following that decision, moreover, there has been a steady and significant increase in the sharing of such SARS-CoV-2 pathogen sequence data through GISAID. By September 2020 that number had surpassed more than 115,000 sequences from more than one hundred nations around the world, and at the time of writing that had further increased to more than 740,000 (GISAID, 2021), meaning that genomic sequences for SARS-CoV-2 are now being shared through GISAID at a historically unprecedented rate (WHO, 2021: 1). Although a significant proportion of this data comes from a comparatively small number of countries that engage extensively in virus sequencing, the overall volume and geographic spread of the data is sufficiently large to suggest that the GISAID model of bioinformational diplomacy pioneered in the influenza field might also become more widely applicable during other future global health emergencies.

Overall, however, it remains impossible to predict at the time of writing how this emerging field of bioinformational diplomacy will unfold in future. It is still too early in the course of the COVID-19 pandemic to properly evaluate how effective the GISAID data-sharing mechanism will ultimately prove in managing all of the multifaceted

sensitivities and potentially conflicting interests between the various stakeholders involved (WHO, 2021: 58). Even the SARS-CoV-2 data being shared through GISAID now, moreover, is likely to represents only a proportion of all the pathogen genetic sequence data being generated around the world and many such data are today also produced in commercial (rather than public) laboratories, which often consider such data to be commercially proprietary. Others, in turn, continue to prefer older public domain models like GenBank that do not place any additional restrictions on the data, or to submit to multiple platforms simultaneously (Wadman, 2021). Considerable variations also remain in the speed with which data is shared (Cohen, 2021) and some scientists are still waiting to share until at least a pre-print publication has been prepared (WHO, 2021: 58). All the while new models of bioinformational diplomacy continue to emerge due to the magnitude of the COVID-19 pandemic such as the COVID-19 Data Portal recently launched by the European Bioinformatics Institute, the US Centers for Disease Control and Prevention's (CDC) new SARS-CoV-2 Sequencing for Public Health Emergency Response, Epidemiology and Surveillance (SPHERES) consortium and the COVID-19 Genomics UK Consortium. Overall, the field of bioinformational diplomacy is thus far from settled, and it very much remains an evolving field of practice characterised by many unresolved questions, heterogeneous practices and a fragmented patchwork of competing models.

## *The global politics of sequential life*

Beyond those uncertainties, all this ongoing contestation, negotiation and experimentation is evidence of how the rise of genetic sequence data is already beginning to recontour the play of security, power and sovereignty in contemporary world politics. The promissory quality of pathogen genetic sequence data is engendering new *socio-technical imaginaries* in the security domain (Jasanoff and Kim, 2015). The most striking of these is the ambition to seamlessly combine molecular biology and bioinformatics into a new real-time global 'digital immune system'. This would consist of all the amalgamated pathogen sequence data being generated around the world today, in order to improve outbreak surveillance and speed up future outbreak detection (Schatz and Phillippy, 2012). The rise of pathogen sequence data is also introducing new stratifications into the field of international security: there are countries in the world capable now of using sequence data to better secure their populations against health-based threats, while many other countries occupy a much more subaltern position of mostly being asked to freely share their sequence data with the rest of the world (Go, 2016; see Harding, 2011; Helmy et al., 2016; Reardon, 2017). More broadly, all these emergent molecular practices around sequential life are also buttressing the wider field of global health security (Kamradt-Scott, 2015; Rushton, 2019; Rushton and Youde, 2014; Samimian-Darash et al., 2016) by raising awareness about the continual presence of biological danger, and by facilitating enhanced molecular strategies for developing new *medical* countermeasures. The pathogen genetic sequence data being generated inside of scientific laboratories are thus becoming deeply entangled with the wider field of (bio)security (see Hoijtink and Leese, 2019; Vogel et al., 2017).

Furthermore, the rise of this valuable new informational resource is also playing into the international distribution of power. When scientists still needed access to physical specimens of new pathogens, this presented low- and middle-income countries (e.g. Indonesia, Brazil, Mexico, Malaysia, the Philippines) with opportunities to develop new political strategies for resisting their perceived exploitation. Countries like Indonesia, for example, began vociferously asserting their 'viral sovereignty' and started leveraging access to biological samples sourced from inside their territories in return for improved access to accruing benefits like new medical interventions (Sedyaningsih et al., 2008; Servick, 2016). Over the past decade, this strategy has triggered the need for formal diplomatic activity, including lengthy and high-level intergovernmental negotiations leading to new multilateral agreements governing the equitable international sharing of resulting benefits. Those include the Nagoya Protocol on Access and Benefit Sharing and the Pandemic Influenza Preparedness (PIP) Framework (Rourke, 2019; Sedyaningsih et al., 2008; Servick, 2016). The PIP Framework, for example, requires that commercial industries benefiting from access to influenza virus samples now make significant financial contributions (through the PIP Secretariat) to this framework. These additional funds can then be used to facilitate technology transfer and capacity building in LMICs. The PIP framework also entails further provisions to ensure that during any future flu pandemic a proportion of – usually quite scarce – pandemic vaccines will be explicitly reserved for affected countries (rather than allowing these to flow almost exclusively to high-income countries).

Pathogen genetic sequence data, however, is widely regarded as falling outside the scope of those existing multilateral agreements. The hard-fought diplomatic frameworks governing the international sharing of benefits derived from genetic resources were mostly negotiated on the basis of still having to exchange biological materials, that is, physical samples of viruses and other microbes (Halabi, 2019; Hinterberger and Porter, 2015). As sequence data become an increasingly powerful informational resource, it remains unclear what options will remain for LMICs to secure more equitable access to the benefits accruing from 'their' genetic resources in future (Fearnley, 2020). There is growing uncertainty as to whether they will be able to develop other diplomatic strategies moving forward, or whether their negotiating positions will ultimately become eroded due to the emergence of pathogen sequence data. Here, then, the rise of genetic sequence data is also already beginning to have significant *power* effects in the international system that are associated with shifting from the exchange of biological specimens to increasingly *informational* exchanges in the sequential management of outbreaks, particularly how the rise of sequence data is re-contouring (often already asymmetric) power relations between high- and low-income countries.

Ultimately, these wider international political impacts of pathogen genetic sequence data are even bleeding into the domain of sovereignty by raising deeper questions about whether governments can retain sovereign control over genetic resources located within their borders (Hinterberger and Porter, 2015). Only recently, for example, a US company managed to patent a new Ebola medicine developed solely on the basis of digital sequence data deposited in the public database GenBank, thus bypassing any international benefit-sharing obligations that would have likely accrued if using material samples sourced from a foreign country (Hammond, 2019). The prospect that the rise of sequence data

could eventually lead many LMIC governments to lose effective control over 'their' genetic resources has triggered the diplomatic need for additional intergovernmental negotiations about how to also handle ownership of such sequence data (and any associated intellectual property) moving forward. These formal diplomatic negotiations have now commenced within the context of the PIP Framework and the Nagoya Protocol. Thus, the *informal* diplomatic practices of life scientists exchanging newly generated pathogen genetic sequence data across national borders have also triggered the need for new *formal* diplomatic negotiations between governments about how to handle such sequence data during future global health emergencies. In the end, the practices of rendering life into legible molecular sequence unfolding inside of scientific laboratories also cascade upwards into the macro-political play of security, power and sovereignty in international relations: *the global politics of sequential life*.

## Conclusion

This article investigated the growing international political significance becoming attached to bioinformation especially in the context of global health emergencies. While it has focused on just one such type of bioinformation, there are evidently also many other kinds of bioinformation similarly becoming more critical to the effective management of outbreaks in the 21st century (Holzscheiter and van Panhuis, 2016). These include various types of epidemiological data used for tracking the geographic and demographic spread of a disease over time. It further includes scientific data about the detailed protein structures of emergent pathogens, as these data too can now be used to better understand their transmission and to identify new drug targets. It also includes clinical trial data about the safety and effectiveness of new medical interventions, which is becoming more significant as governments seek to develop biomedical interventions to protect their populations against new outbreaks. It cannot be assumed that existing data-sharing sensitivities will be identical across different types of data, nor that sharing practices effective for one kind of bioinformation will be effective for all other types as well. There are, moreover, additional challenges triggered by the urgent need to also better integrate all these diverse types of bioinformation, and the concomitant 'platformization' of data sharing mechanisms, that is, trying to move those systems from a position of hosting fairly rudimentary sequence databases, towards building much broader platforms capable of interfacing many different actors using such data for further processing (Helmond, 2015). All the while, many of the difficulties experienced so starkly in relation to outbreaks are also beginning to spill over into more routine forms of international scientific research as well. Thus, there remains much about bioinformational diplomacy that we still do *not* know, and that will require further study in future.

Just from analysing pathogen genetic sequence data, however, it is apparent that state sovereignty is already becoming much more closely tethered to the capacity of governments to access and control such bioinformational flows (Hinterberger and Porter, 2015; see also Stephenson, 2011). Like other key areas of International Relations, including the conduct of war (see Cooper, 2008; Dillon and Reid, 2009), the management of global health emergencies is undergoing a protracted process of informationalisation. Bioinformation too now forms an integral part of what the information philosopher

Luciano Floridi calls the global 'infosophere', that is, the dense 'informational environment constituted by all informational entities, their properties, interactions, processes and mutual relations' within which states are now embedded (Floridi, 2014: 41). The emergence of such bioinformation – its process of *in-form-ation* – is already triggering new constellations, networks and hierarchies in the international system; and the power of states in the international order increasingly depends upon their capacity to rapidly generate, access and evaluate different flows of information. Here, then, the rise of bioinformational diplomacy requires scholars to broadly re-think *international* relations also as *informational* relations.

The nascent field of bioinformational diplomacy additionally reveals something about the changing nature of 21st century diplomacy. It shows that beneath the level of formal intergovernmental diplomacy widely familiar to scholars of International Relations, there also lurks another thick layer of more informal and second-order diplomacy: the epistemic diplomacy routinely conducted by life scientists. In *Science in Action* Bruno Latour described the everyday material practices taking place inside of scientific laboratories. This eventually culminated in the development of actor-network theory (ANT), but also produced many insights about the intricate workings of scientific practice including his comparatively lesser known notion of 'centres of calculation'. Latour had observed that scientists are in fact critically dependent upon the global circulatory movement and international accumulation of a wide variety of knowledge resources sourced from all around the world such as 'specimens, maps, diagrams, logs, questionnaires and article forms of all sorts' that are then assembled and concentrated in leading laboratories or 'centres of calculation' (Latour, 1987: 232). Without access to those international resources, scientists would be unable carry out their work. The study of bioinformational diplomacy suggests that those international cycles of scientific accumulation today also span pathogen genetic sequence data, and that scientists must therefore continually develop, sustain and buttress various informal strategies to globally source this vital bioinformation across sensitive international and geopolitical divides.

In the second instance, the rise of bioinformational diplomacy thus intimates that scientists too must be considered as a particular type, or class, of informal diplomatic actors in the contemporary international system. Scientists do not just contribute their epistemic expertise to formal diplomatic processes that require specialist knowledge inputs; they themselves must also continually develop a plethora of more infra-diplomatic practices to globally access the valuable epistemic resources so essential for their own work. What, then, are the other informal mechanisms and strategies of epistemic diplomacy utilised by scientists to internationally source the diverse knowledge resources that they need for conducting their investigations especially across sensitive international divides? How do these informal practices seek to navigate and potentially circumvent burdensome bureaucratic requirements, national regulations and/or existing international agreements? How, moreover, can these the more informal practices of scientists potentially also trigger the need for significant adjustments to government practice, diplomatic arrangements and international law? These more informal and infra-diplomatic efforts routinely undertaken by scientists too deserve more scholarly attention.

Finally, the emerging field of bioinformational diplomacy also challenges scholars of International Relations to begin thinking differently about the underlying relationship between international relations and the life sciences. Recent years have seen increased scholarly interest in the relationship between science and international politics (see Bosquet, 2010; Hoijtink and Leese, 2019; Vogel et al., 2017) giving rise to a new scholarly subfield of science diplomacy (Domingues, 2019; Flink and Rüffin, 2019; Kaltofen and Acuto, 2018). This scholarly field of science diplomacy is heavily influenced by the tri-partite conception of science diplomacy advanced in the report on *New Frontiers in Science Diplomacy*, jointly published in 2010 by the U.K. Royal Society and the American Association for the Advancement of Science (Royal Society, 2010). The report outlines three major ways in which the relationship between science and diplomacy can be conceptualised: (1) *diplomacy for science* – how diplomacy can facilitate international scientific cooperation; (2) *science in diplomacy* – how scientists can inform foreign policy through generating scientific evidence and new technologies; and (3) *science for diplomacy* – using scientific collaboration as a seemingly neutral area though which to improve fraught interstate relations. Throughout this influential report, science and diplomacy are thus considered as distinct professional fields that can be put into the instrumental service of one another.

The rise of bioinformational diplomacy challenges and problematises this prominent view. Through the in-depth study of bioinformational diplomacy it has been possible to carefully trace how the sequencing of life at tiny molecular scale undertaken inside of scientific laboratories also ends up recontouring the macro-political play of security, power and sovereignty in international relations. Rather than thinking about science and diplomacy as largely separate domains that can be put into instrumental service of one another, the rise of bioinformational diplomacy instead points towards a far more deeply entangled, and even constitutive, relationship between the life sciences and international relations. Moving forward, there is thus also a need to explore what other kinds of scientific practice, in biology but also beyond, are similarly becoming constitutive of new international relations today like quantum physics, the neuro-sciences, the nano-sciences, and so forth. For we cannot come to know the 'international' properly, without also studying science.

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